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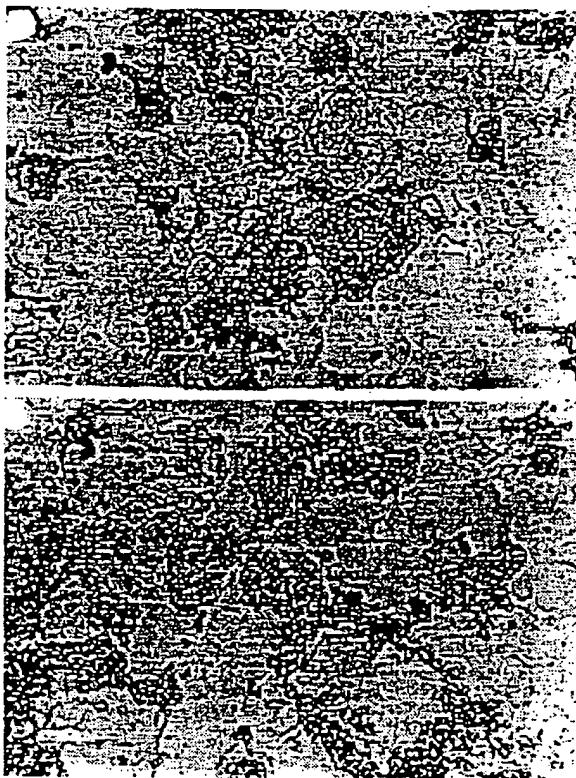
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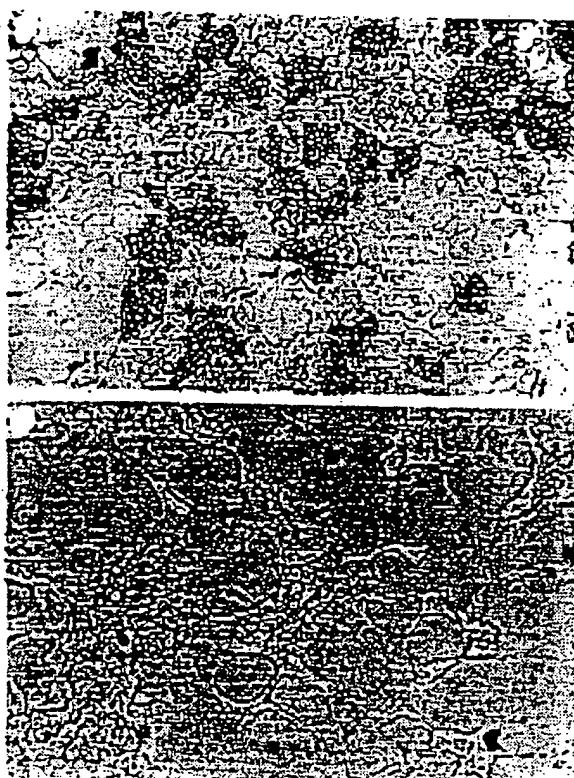
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**FIGURE 1**

**FIG. 1a**



**FIG. 1b**

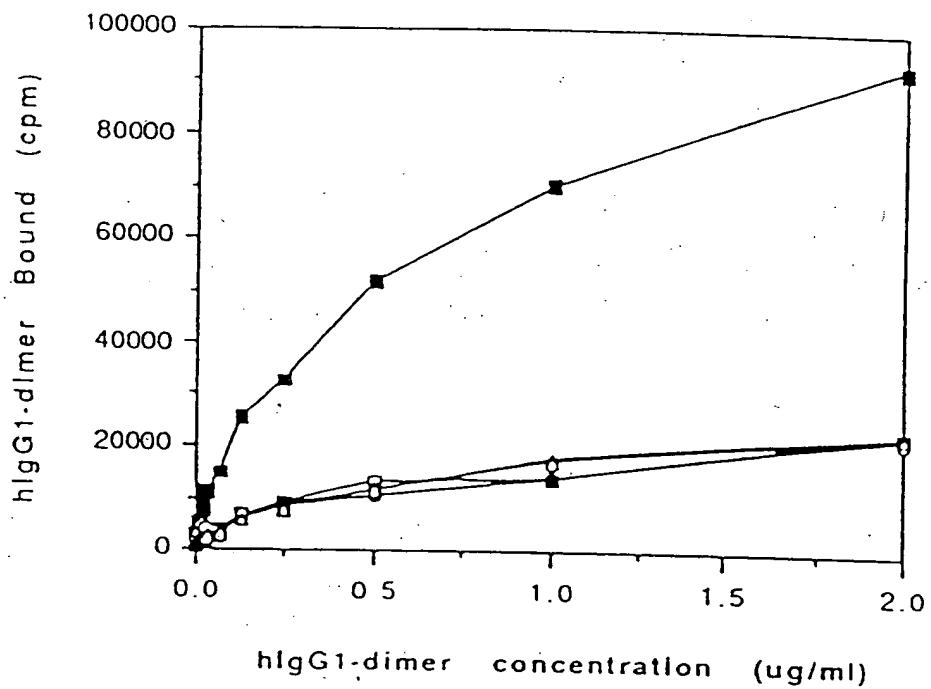


**FIG. 1c**

**FIG. 1d**

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FIGURE 2



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FIGURE 3

FIG. 3b

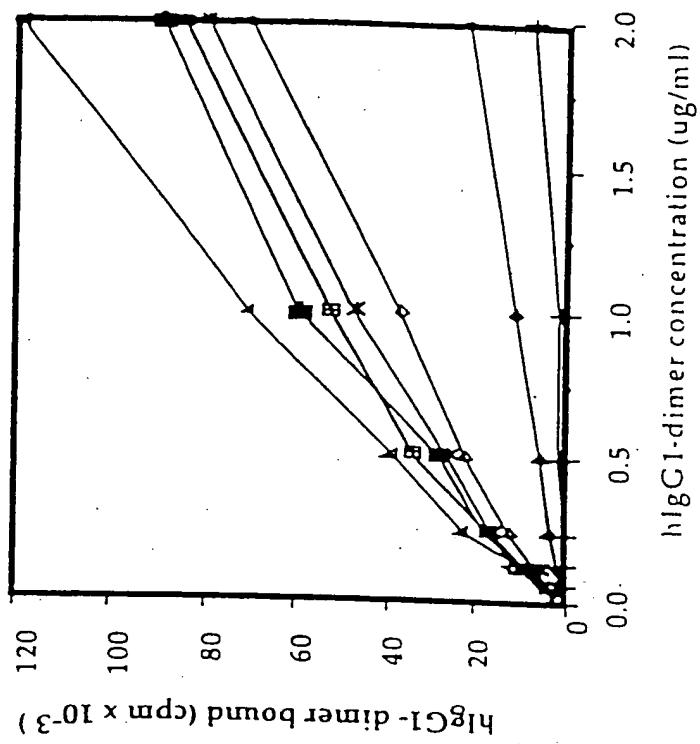


FIG. 3a

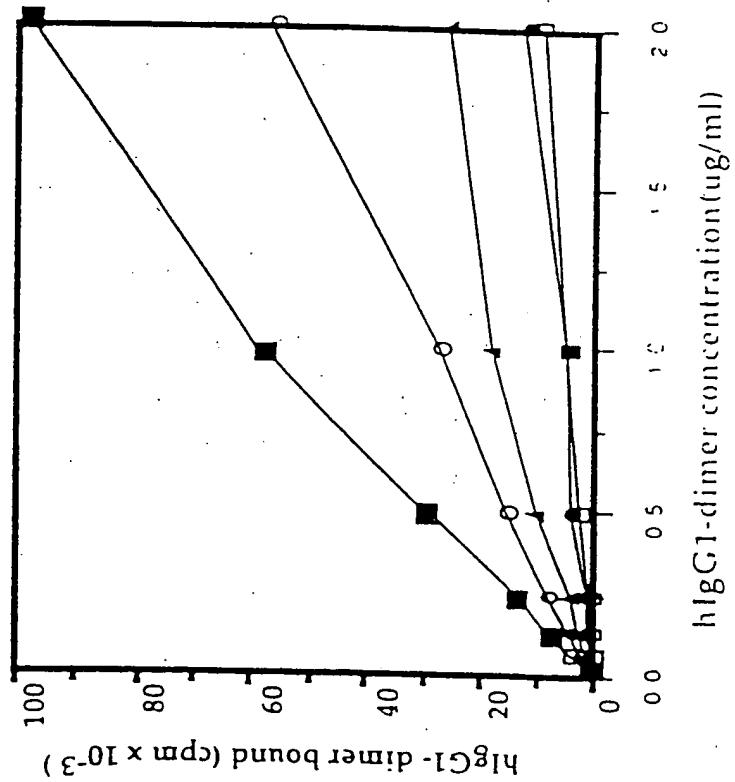
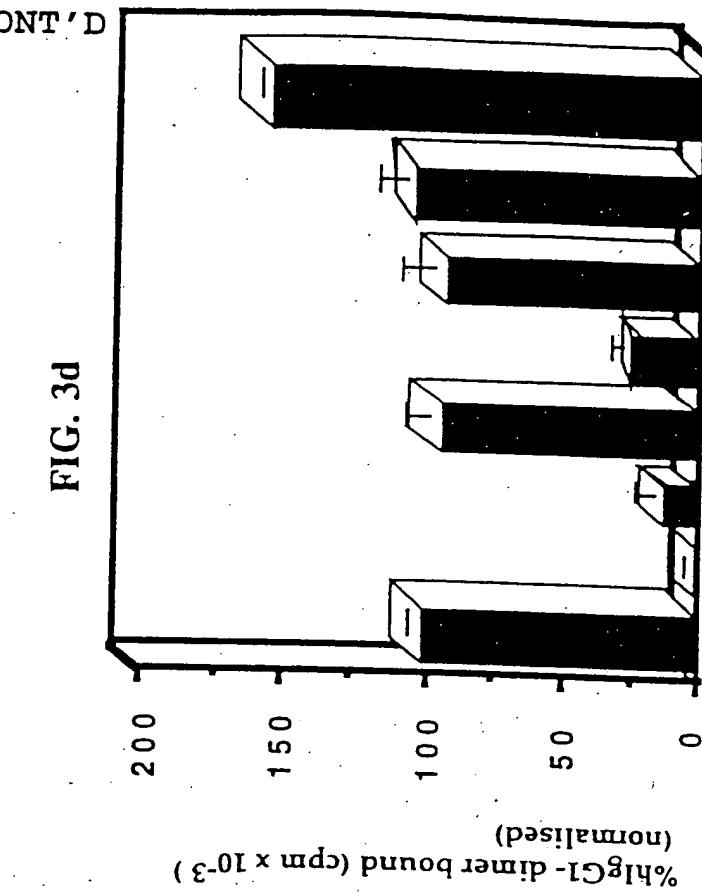
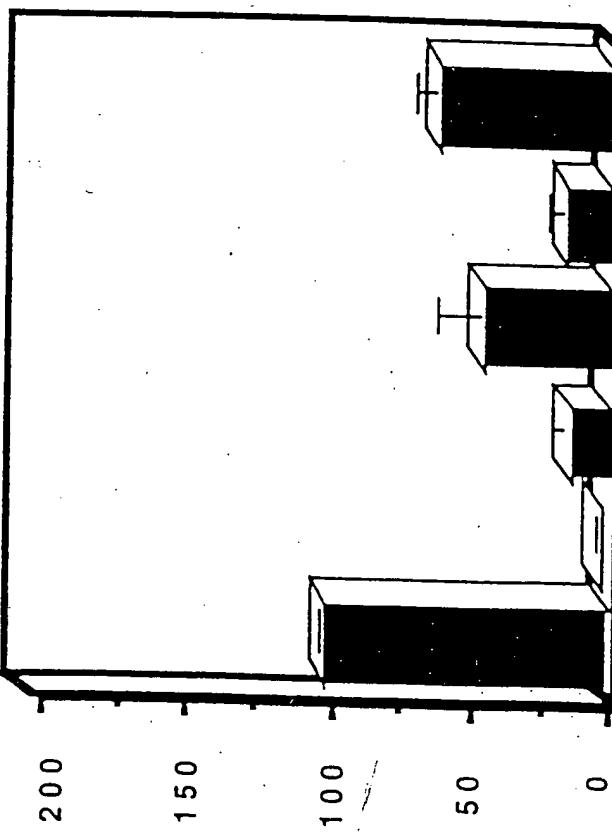


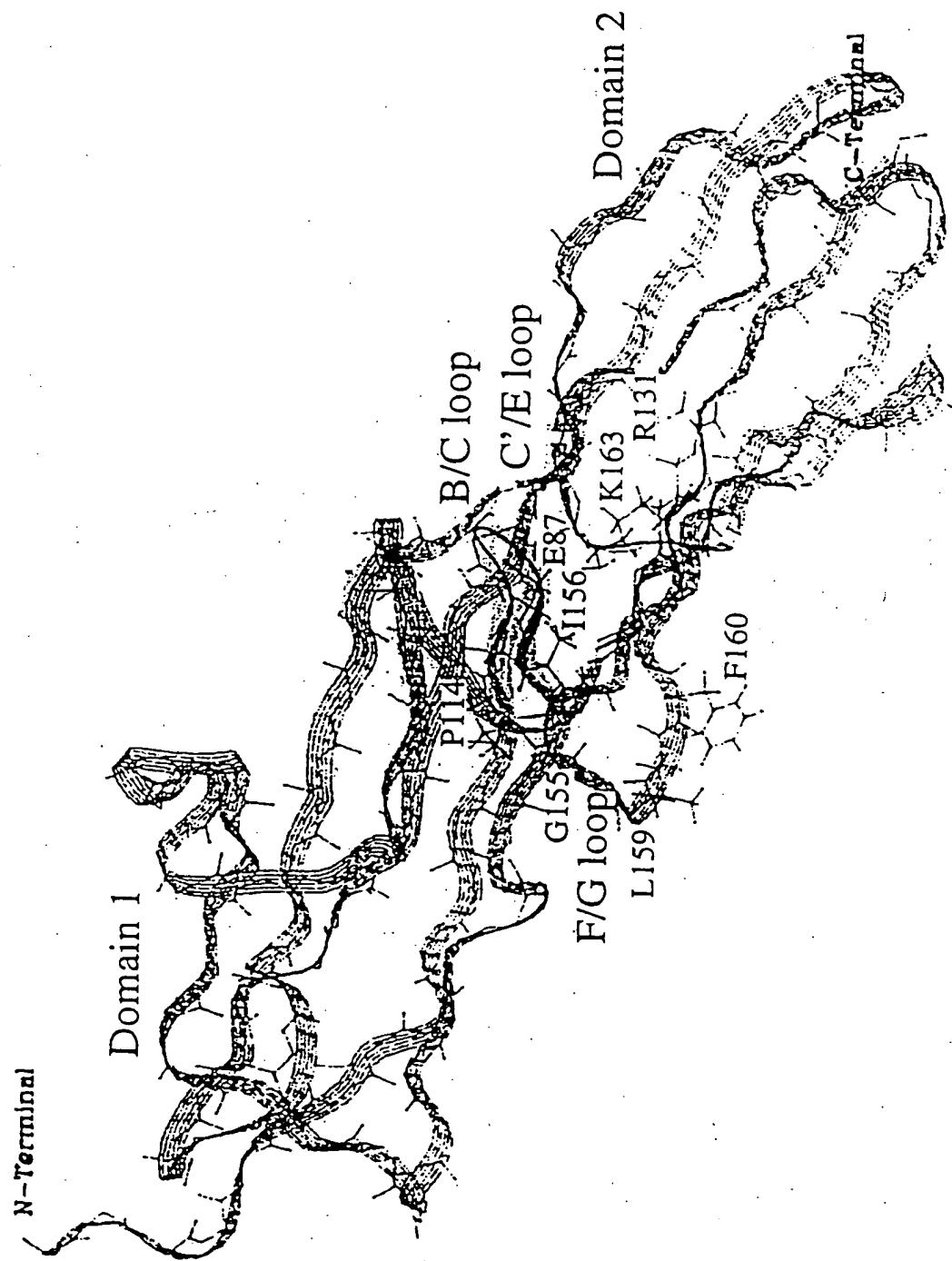
FIGURE 3 CONT'D

FIG. 3d  
FIG. 3c

Construct	hIgG1-dimer bound (cpm x 10 <sup>-3</sup> )
WT	100
FcεRII	129
FcεRIII	130

Construct	hIgG1-dimer bound (cpm x 10 <sup>-3</sup> )
WT	100
FcεRII	113
FcεRIII	114

FIGURE 4



**FIGURE 5**huFc<sub>RI</sub> chain C'-E, F-G loop Ala mutant oligo nucleotides

## F-G loop

5

e154 (Lys) <sup>④</sup> Ala EFG-01+EFG-02

EFG-01: 5' CTGTACGGCGCAGTGTGGCAGC 3'

EFG-02: 5' GCTGCCACACTGCGCCCGTACAG 3'

10 e155 (Val) <sup>④</sup> Ala EFG-03+EFG-04

EFG-03: 5' GTACCGGCAAAGCATGGCAGCTGG 3'

EFG-04: 5' CCAGCTGCCATGCTTGCCCCGTAC 3'

e156 (Trp) <sup>④</sup> Ala EFG-05+EFG-06

15 EFG-05: 5' GGGCAAAGTGGCACAGCTGGAC 3'

EFG-06: 5' GTCCAGCTGTGCCACTTGGCCC 3'

e157 (Gln) <sup>④</sup> Ala EFG-07+EFG-08

EFG-07: 5' GCAAAGTGTGGGCACTGGACTATG 3'

20 EFG-08: 5' CATA GTCCAGTGCCACACTTGC 3'

e158 (Leu) <sup>④</sup> Ala EFG-09+EFG-10

EFG-09: 5' GTGTGGCAGGCAGACTATGAGTC 3'

EFG-10: 5' GACTCATAGTCTGCCACAC 3'

25

e159 (Asp) <sup>④</sup> Ala EFG-11+EFG-12

EFG-11: 5' GTGGCAGCTGGCATATGAGTCTG 3'

EFG-12: 5' CAGACTCATATGCCAGCTGCCAC 3'

30 e160 (Tyr) <sup>④</sup> Ala EFG-13+EFG-14

EFG-13: 5' GCAGCTGGACGCAGAGTCTGAGC 3'

EFG-14: 5' GCTCAGACTCTGCCAGCTGC 3'

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## Figure 5 cont.

e161 (Glu)  $\circledast$  Ala EFG-07+EFG-08

EFG-15: 5' GCTGGACTATGCATCTGAGCCCC 3'

EFG-16: 5' GGGGCTCAGATGCATAGTCCAGC 3'

## 5 C'-E loop

e129 (Tyr)  $\circledast$  Ala EBS-01+EBS-02

EBS-01: 5' GCTCTCAAGGCATGGTATGAGAAC 3'

EBS-02: 5' GTTCTCATACCATGCCTTGAGAGC 3'

10

e130 (Trp)  $\circledast$  Ala EBS-03+EBS-04

EBS-03: 5' CTCAAAGTACGCATATGAGAACAC 3'

EBS-04: 5' GTGGTTCTCATATGCGTACTTGAG 3'

15 e131 (Tyr)  $\circledast$  Ala EBS-01+EBS-02

EBS-05: 5' CAAGTACTGGGCAGAGAACAC 3'

EBS-06: 5' GTGGTTCTCTGCCAGTACTTG 3'

e132 (Glu)  $\circledast$  Ala EBS-07+EBS-08

20 EBS-07: 5' GTACTGGTATGCAAACACAAACATC 3'

EBS-08: 5' GATGTTGTGGTTGCATACCACTAC 3'

e133 (Asn)  $\circledast$  Ala EBS-09+EBS-10

EBS-09: 5' CTGGTATGAGGCACACAAACATCTCC 3'

25 EBS-10: 5' GGAGATGTTGTGCCTCATACCAAG 3'

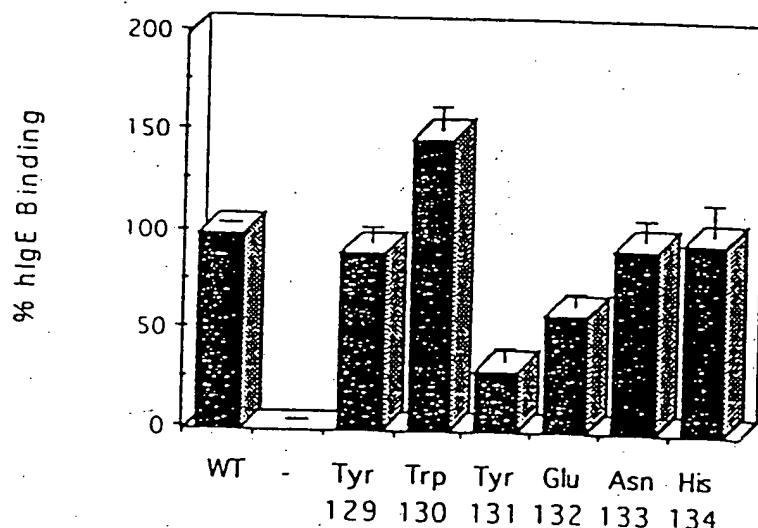
e134 (His)  $\circledast$  Ala EBS-11+EBS-12

EBS-11: 5' GGTATGAGAACGCAAACATCTCCATTAC 3'

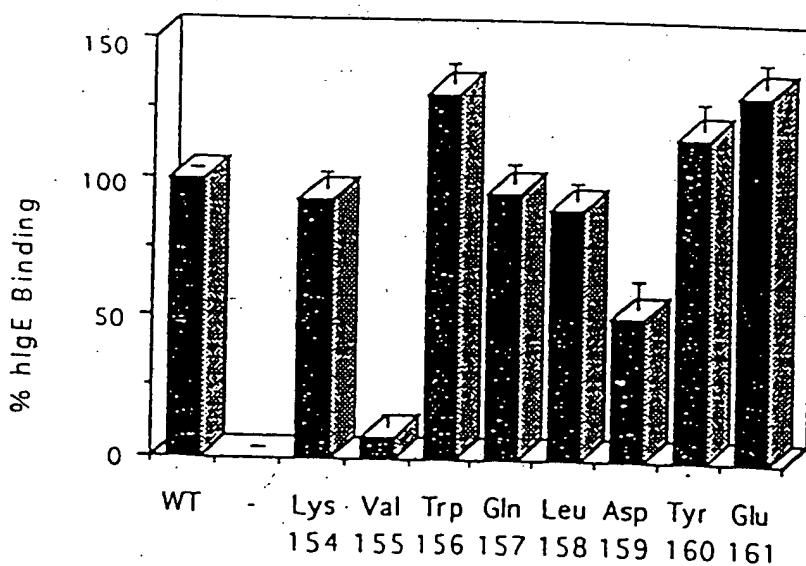
EBS-12: 5' GTAATGGAGATGTTGCGTTCTCATACC 3'

FIGURE 6

Effect of mutation of the IgE receptor (Fc $\epsilon$ RI) on the binding of IgE  
C'-E LOOP



## F-G LOOP



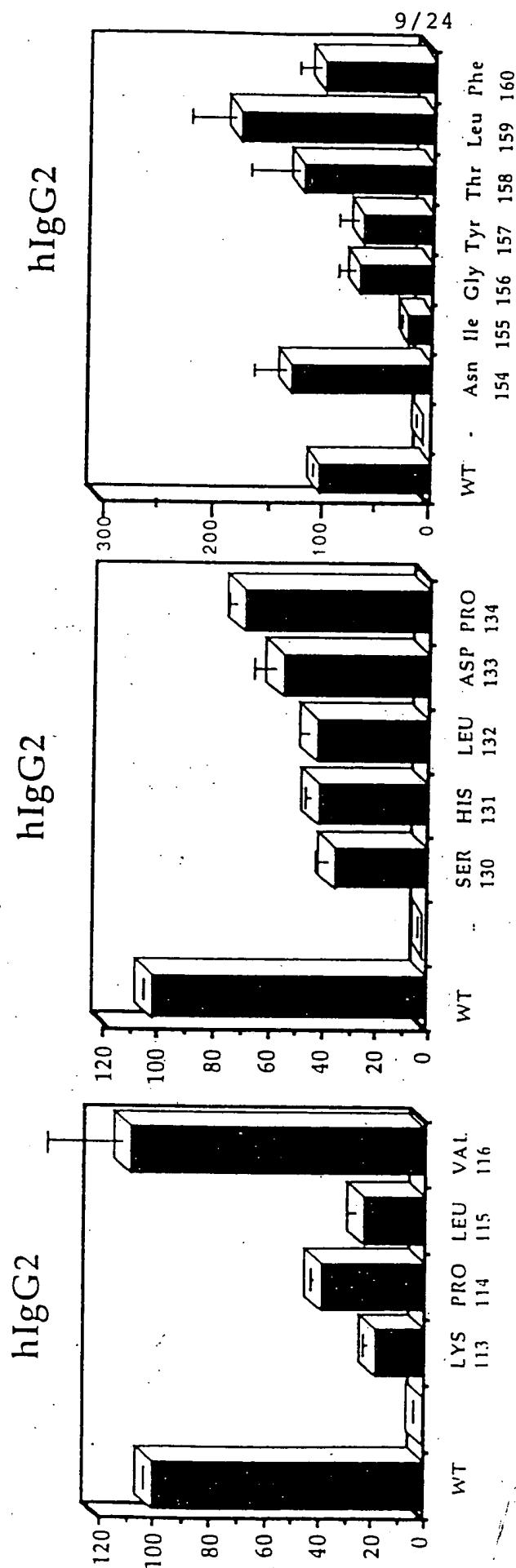


FIGURE 7

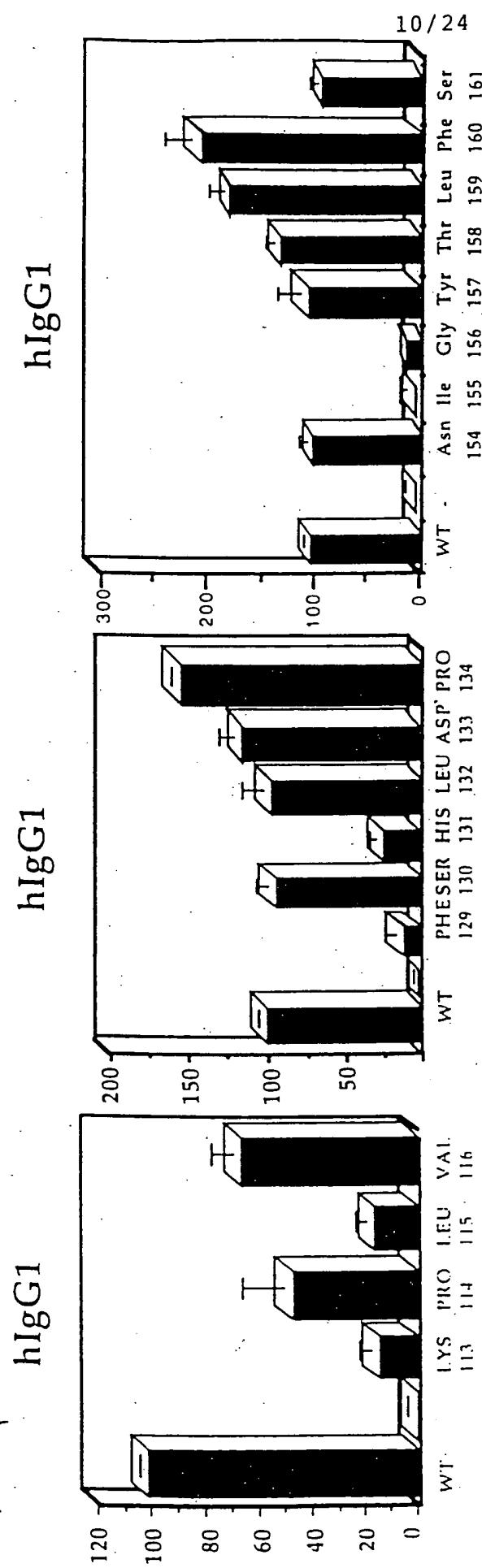
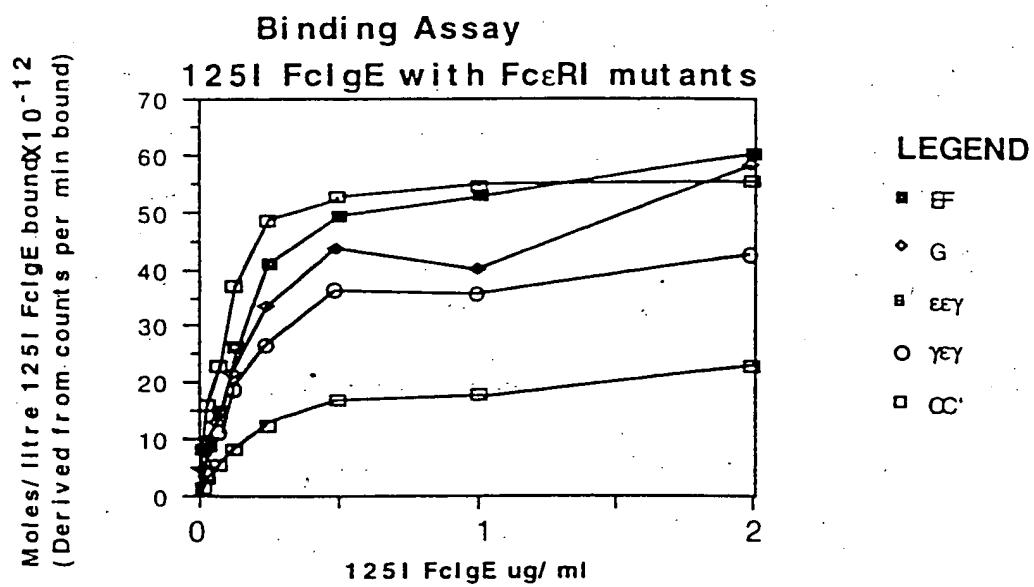


FIGURE 7 CONT'D..

**FIGURE 8**

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**FIGURE 9**

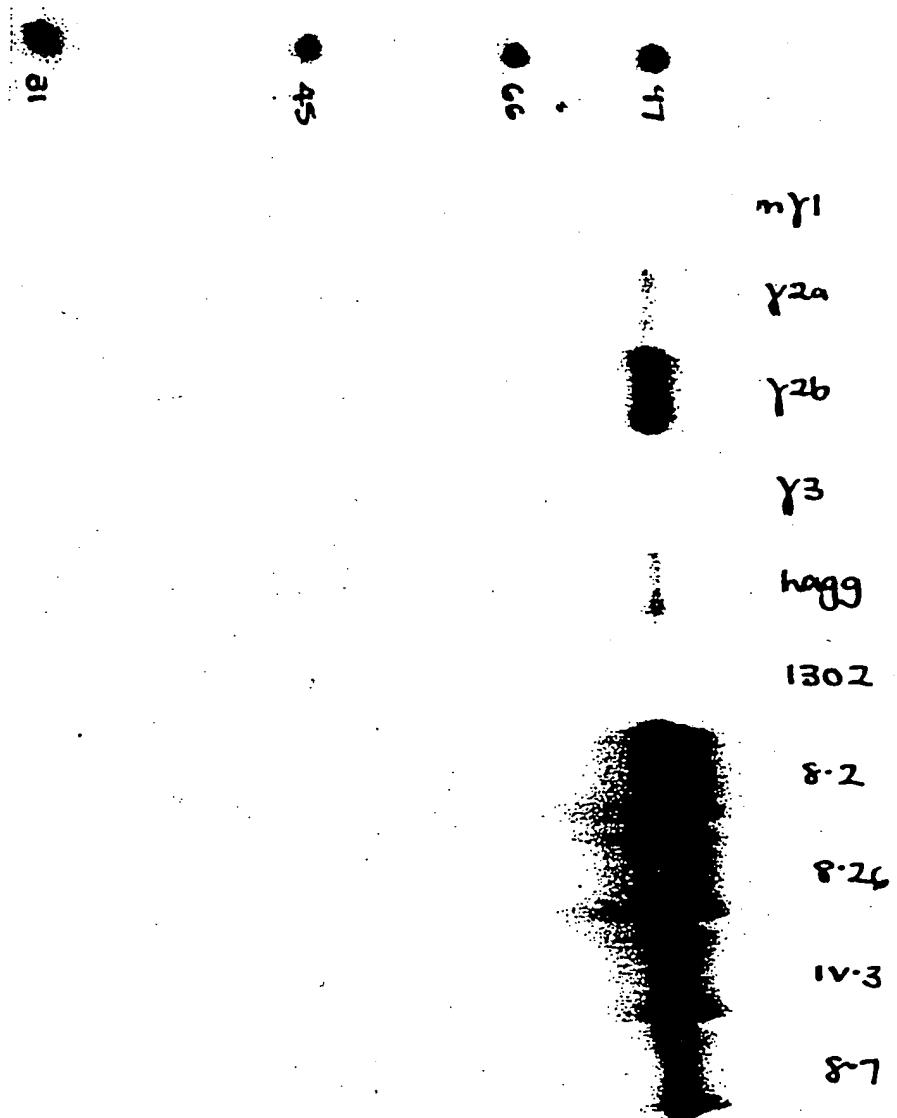


FIGURE 10

FIG. 10 A Blood Clearance of HSA-FcgRII and FcgRII

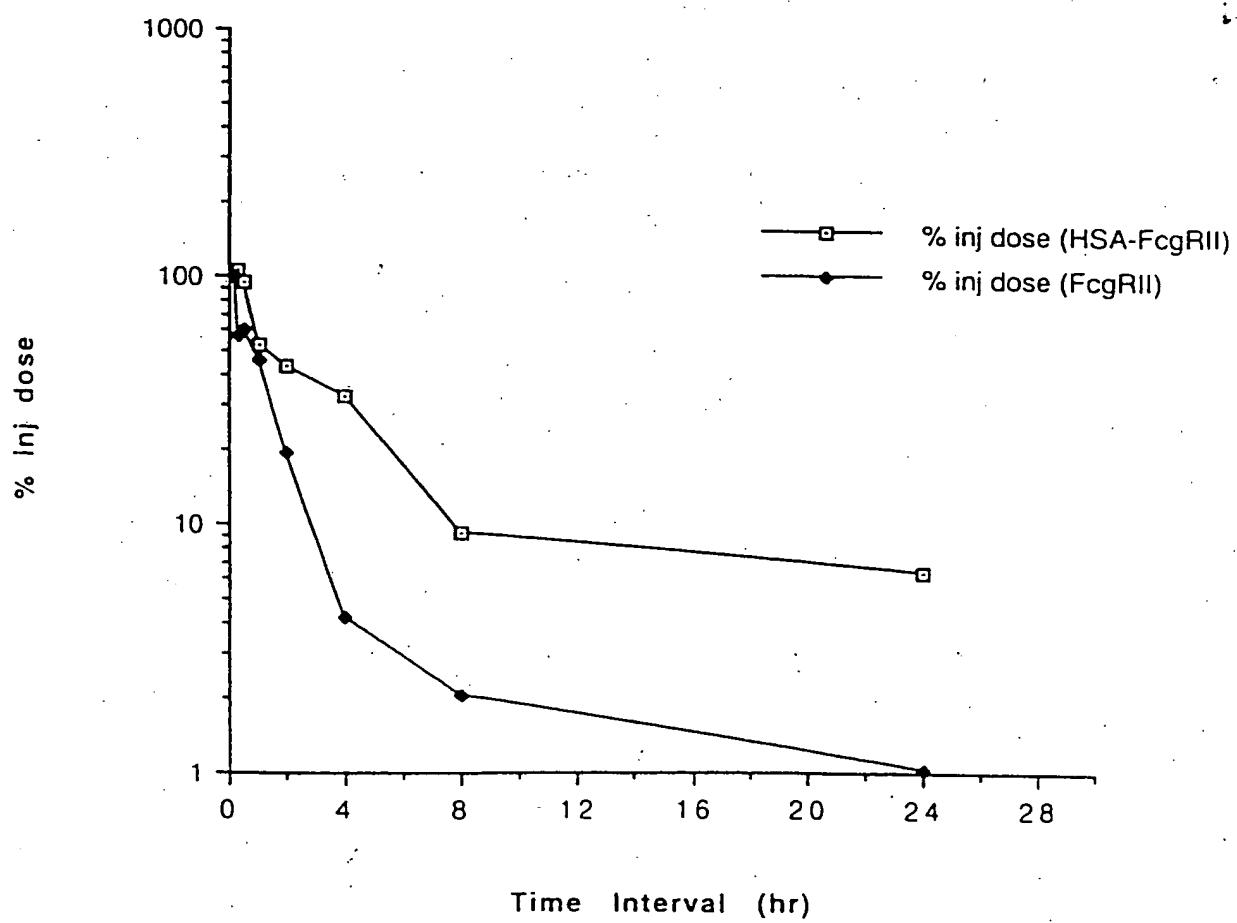


FIGURE 10 CONT'D..

FIG.10  
**B**

## Urine accumulated v's time

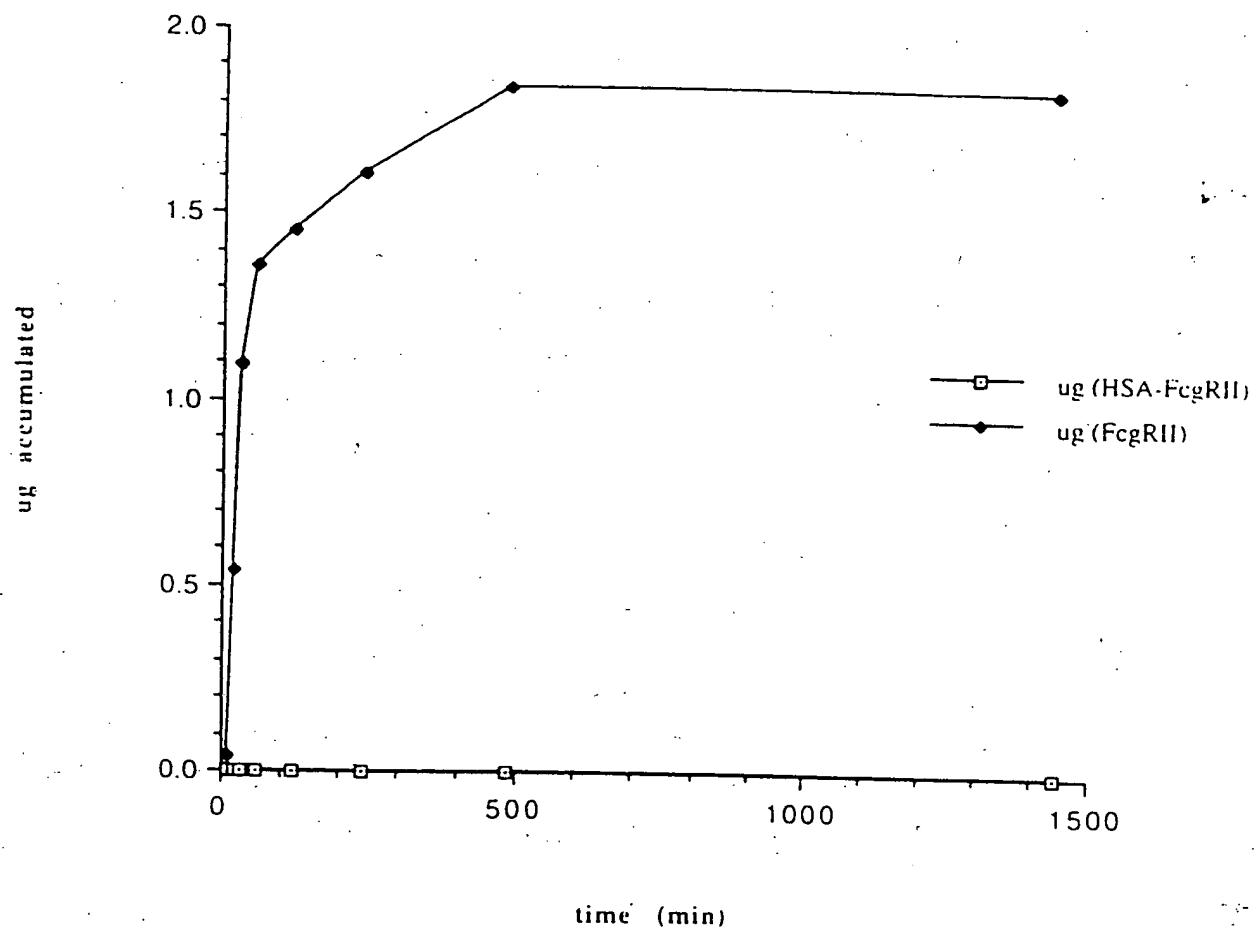


FIGURE 11

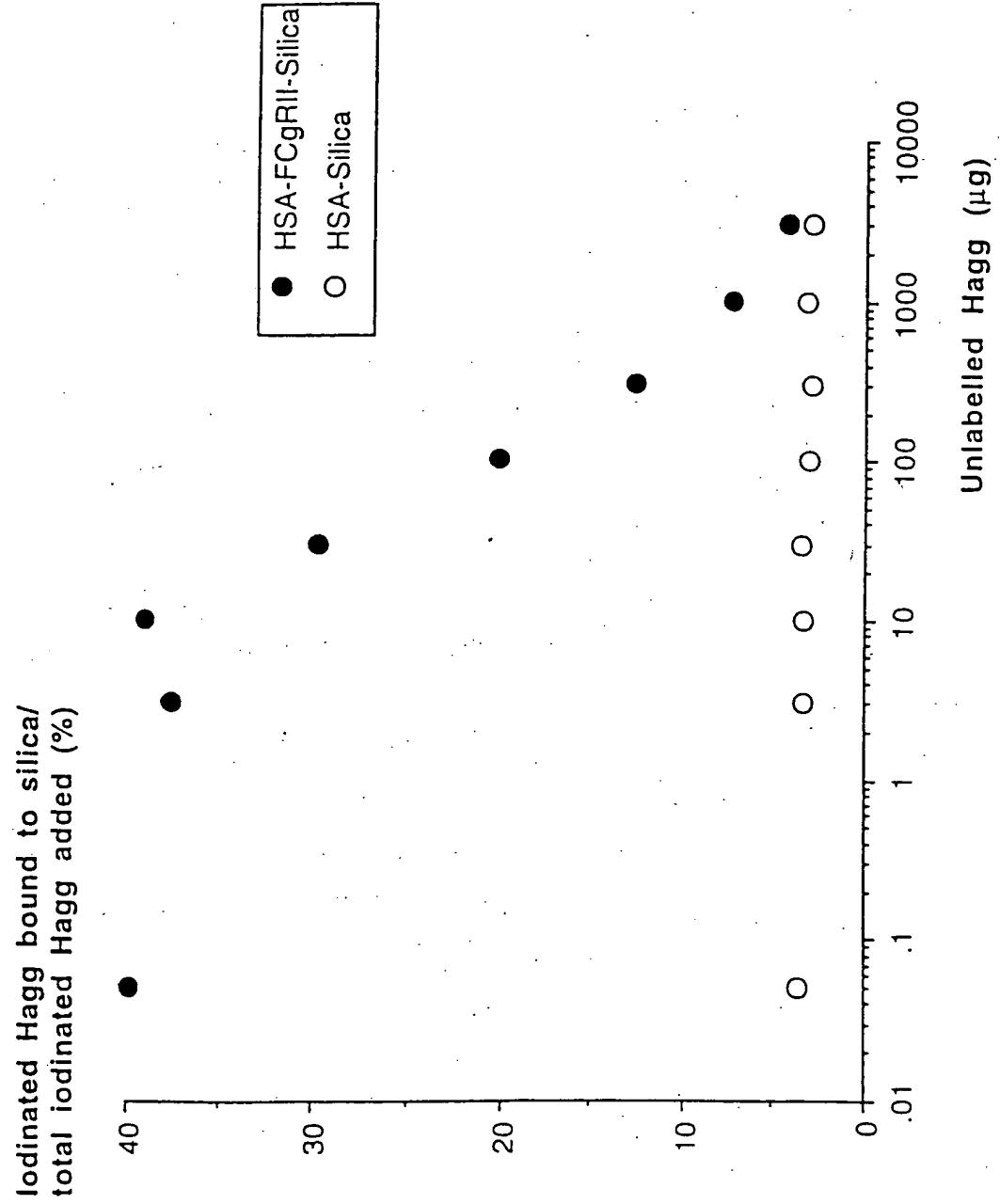


FIGURE 12

16/24

1/1

31/11

GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA  
 asp ala his lys ser glu val ala his arg phe lys asp leu gly glu glu asn phe lys  
 61/21 91/31

GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA  
 ala leu val leu ile ala phe ala gln tyr leu gln gln cys pro phe glu asp his val  
 121/41 151/51

AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA  
 lys leu val asn glu val thr glu phe ala lys thr cys val ala asp glu ser ala glu  
 181/61 211/71

AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT  
 asn cys asp lys ser leu his thr leu phe gly asp lys leu cys thr val ala thr leu  
 241/81 271/91

CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GAG AGA AAT GAA  
 arg glu thr tyr gly glu met ala asp cys cys ala lys gln glu pro glu arg asn glu  
 301/101 331/111

TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT  
 cys phe leu gln his lys asp asp asn pro asn leu pro arg leu val arg pro glu val  
 361/121 391/131

GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT  
 asp val met cys thr ala phe his asp asn glu glu thr phe leu lys lys tyr leu tyr  
 421/141 451/151

GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG  
 glu ile ala arg arg his pro tyr phe tyr ala pro glu leu leu phe phe ala lys arg  
 481/161 511/171

TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA  
 tyr lys ala ala phe thr glu cys cys gln ala ala asp lys ala ala cys leu leu pro  
 541/181 571/191

AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT  
 lys leu asp glu leu arg asp glu gly lys ala ser ser ala lys gln arg leu lys cys  
 601/201 631/211

GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC  
 ala ser leu gln lys phe gly glu arg ala phe lys ala trp ala val ala arg leu ser  
 661/221 691/231

CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA  
 gln arg phe pro lys ala glu phe ala glu val ser lys leu val thr asp leu thr lys  
 721/241 751/251

GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT  
 val his thr glu cys cys his gly asp leu leu glu cys ala asp asp arg ala asp leu  
 781/261 811/271

GCC AAG TAT ATC TGT GAA AAT CAA GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA  
 ala lys tyr ile cys glu asn gln asp ser ile ser ser lys leu lys glu cys cys glu  
 841/281 871/291

AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT  
 lys pro leu leu glu lys ser his cys ile ala glu val glu asn asp glu met pro ala  
 901/301 931/311

GAC TTG CCT TCA TTA GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT  
 asp leu pro ser leu ala ala asp phe val glu ser lys asp val cys lys asn tyr ala  
 961/321 991/331

GAG GCA AAG GAT GTC TTC CTG GGC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT  
 glu ala lys asp val phe leu gly met phe leu tyr glu tyr ala arg arg his pro asp  
 1021/341 1051/351

TAC TCT GTC GTG CTG CTG AGA CTT GCC AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC  
 tyr ser val val leu leu leu arg leu ala lys thr tyr glu thr thr leu glu lys cys  
 1081/361 1111/371

TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CTT  
 cys ala ala ala asp pro his glu cys tyr ala lys val phe asp glu phe lys pro leu  
 1141/381 1171/391

GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAT TGT GAG CTT TTT GAG CAG CTT GGA GAG  
 val glu glu pro gln asn leu ile lys gln asn cys glu leu phe glu gln leu gly glu  
 1201/401 1231/411

TAC AAA TTC CAG AAT GCG CTA TTA GTT CGT TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT  
 tyr lys phe gln asn ala leu leu val arg tyr thr lys lys val pro gln val ser thr  
 1261/421 1291/431

## FIGURE 12 CONT'D...

CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT  
 pro thr leu val glu val ser arg asn leu gly lys val gly ser lys cys cys lys his  
 1321/441  
 1351/451  
 CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA  
 pro glu ala lys arg met pro cys ala glu asp tyr leu ser val val leu asn gln leu  
 1381/461  
 1411/471  
 TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT GAC AGA GTC ACA AAA TGC TGC ACA GAA TCC  
 cys val leu his glu lys thr pro val ser asp arg val thr lys cys cys thr glu ser  
 1441/481  
 1471/491  
 TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA  
 leu val asn arg arg pro cys phe ser ala leu glu val asp glu thr tyr val pro lys  
 1501/501  
 1531/511  
 GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG  
 glu phe asn ala glu thr phe thr phe his ala asp ile cys thr leu ser glu lys glu  
 1561/521  
 1591/531  
 AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT GAG CTC GTG AAA CAC AAG CCC AAG GCA ACA  
 arg gln ile lys lys gln thr ala leu val glu leu val lys his lys pro lys ala thr  
 1621/541  
 1651/551  
 AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCA GCT TTT GTA GAG AAG TGC TGC AAG  
 lys glu gln leu lys ala val met asp asp phe ala ala phe val glu lys cys cys lys  
 1681/561  
 1711/571  
 GCT GAC GAT AAG AAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA  
 ala asp asp lys lys thr cys phe ala glu glu gly lys lys leu val ala ala ser gln  
 1741/581  
 1771/591  
 GCT GCC TTA GGC GCT CCC CCA AAG GCT GTG CTG AAA CTT GAG CCC CCG TGG ATC AAC GTG  
 ala ala leu gly ala pro pro lys ala val leu lys leu glu pro pro trp ile asn val  
 1801/601  
 1831/611  
 CTC CAG GAG GAC TCT GTG ACT CTG ACA TGC CAG GGG GCT CGC AGC CCT GAG AGC GAC TCC  
 leu gln glu asp ser val thr leu thr cys gln gly ala arg ser pro glu ser asp ser  
 1861/621  
 1891/631  
 ATT CAG TGG TTC CAC AAT GGG AAT CTC ATT CCC ACC CAC ACg cAG CCC AGC TAC AGG TTC  
 ile gln trp phe his asn gly asn leu ile pro thr his thr gln pro ser tyr arg phe  
 1921/641  
 1951/651  
 AAG GCC AAC AAC AAT GAC AGC GGG GAG TAC ACG TGC CAG ACT GGC CAG ACC AGC CTC AGC  
 lys ala asn asn asn asp ser gly glu tyr thr cys gln thr gly gln thr ser leu ser  
 1981/661  
 2011/671  
 GAC CCT GTG CAT CTG ACT GTG CTT TCC GAA TGG CTG GTG CTC CAG ACC CCT CAC CTG GAG  
 asp pro val his leu thr val leu ser glu trp leu val leu gln thr pro his leu glu  
 2041/681  
 2071/691  
 TTC CAG GAG GGA GAA ACC ATC ATG CTG AGG TGC CAC AGC TGG AAG GAC AAG CCT CTG GTC  
 phe gln glu gly glu thr ile met leu arg cys his ser trp lys asp lys pro leu val  
 2101/701  
 2131/711  
 AAG GTC ACA TTC TTC CAG AAT GGA AAA TCC CAG AAA TTC TCC CAT TTG GAT CCC ACC TTC  
 lys val thr phe phe gln asn gly lys ser gln lys phe ser his leu asp pro thr phe  
 2161/721  
 2191/731  
 TCC ATC CCA CAA GCA AAC CAC AGT CAC AGT GGT GAT TAC CAC TGC ACA GGA AAC ATA GGC  
 ser ile pro gln ala asn his ser his ser gly asp tyr his cys thr gly asn ile gly  
 2221/741  
 2251/751  
 TAC ACG CTG TTC TCA TCC AAG CCT GTG ACC ATC ACT GTC CAA TAG  
 tyr thr leu phe ser ser lys pro val thr ile thr val gln AMB

FIGURE 13

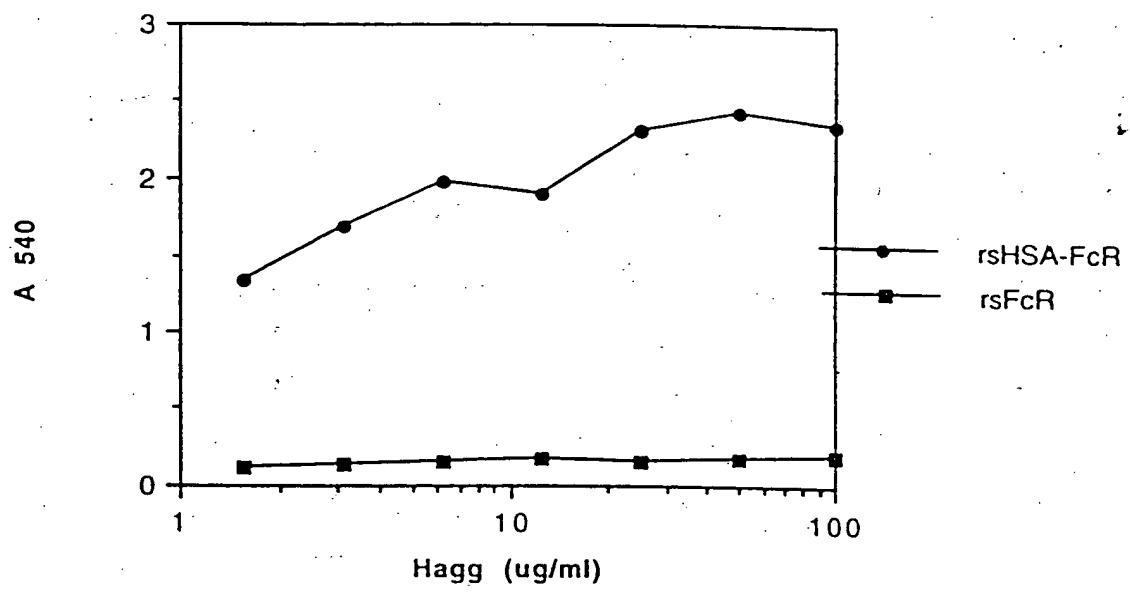
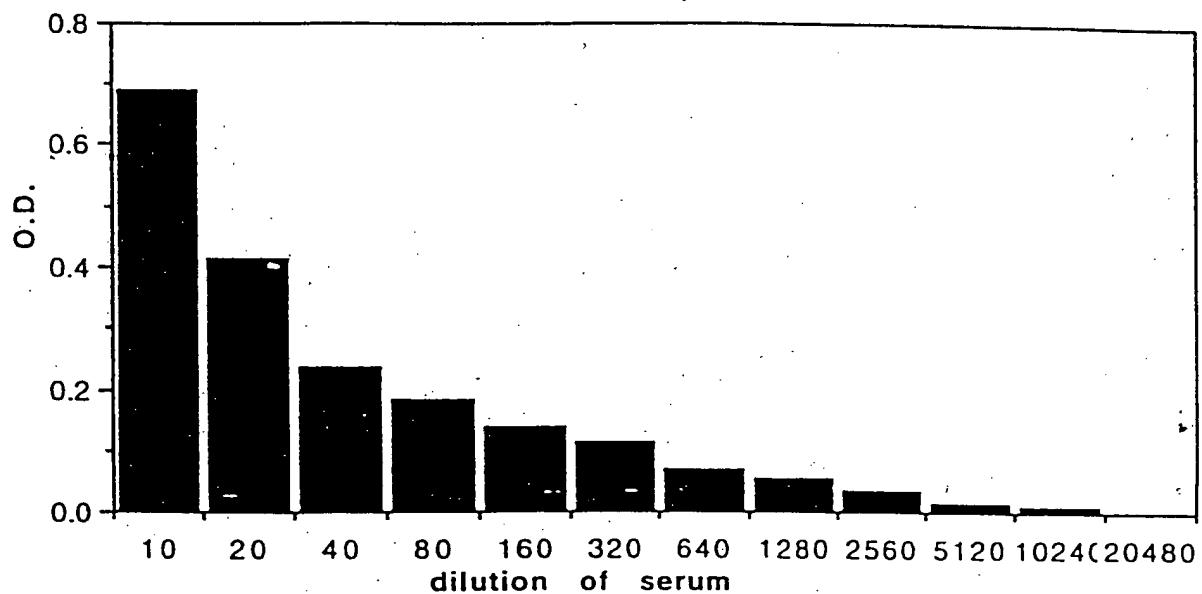


FIGURE 14

Coated with anti-  $Fc\gamma RII$  antibody

not Ab coated

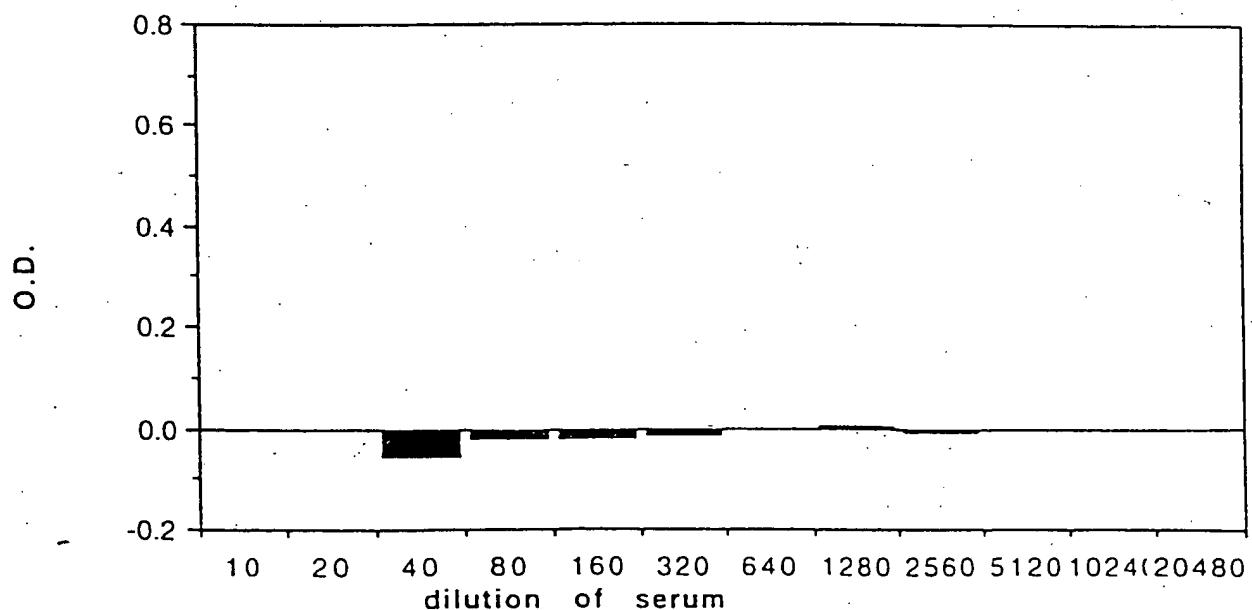


FIGURE 15

## Depletion of Heat aggregated Ig (Hagg) using FcgRII-HSA silica

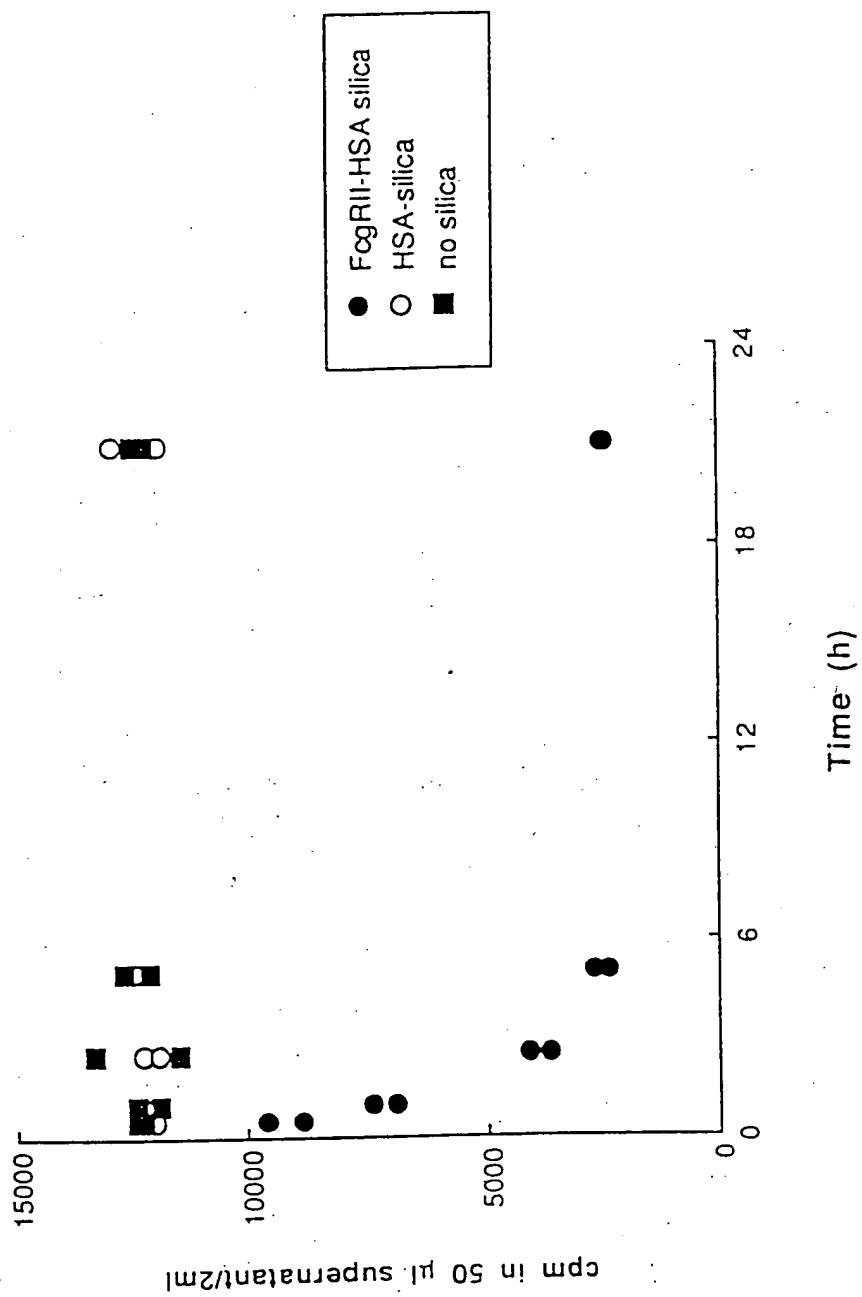


FIGURE 16

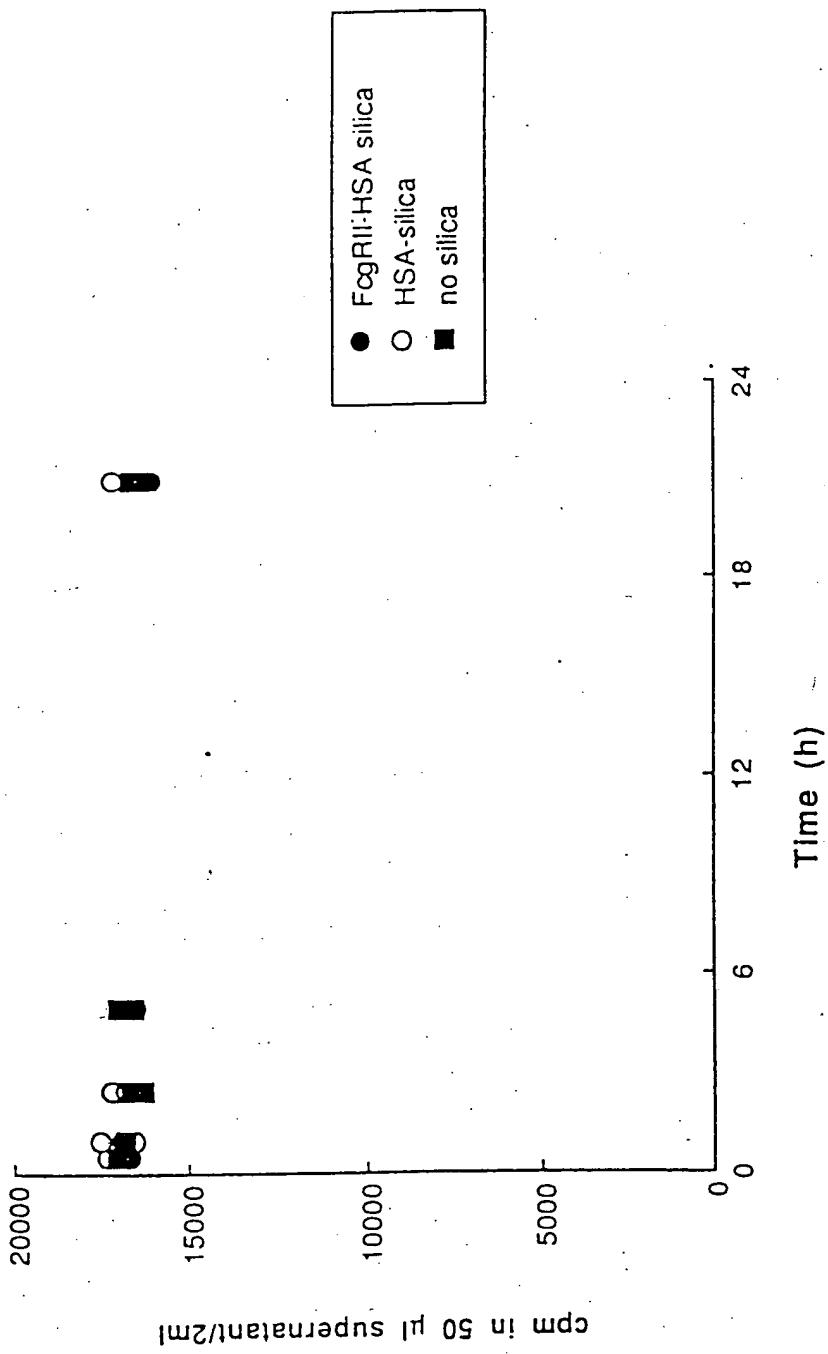
No depletion of monomeric Ig using Fc<sub>γ</sub>RII-HSA silica

FIGURE 17

Functional soluble Fc $\gamma$ RII detected binding to hagg using the MoAb 8.2

**Titration of rsFc $\gamma$ RII from various sources**

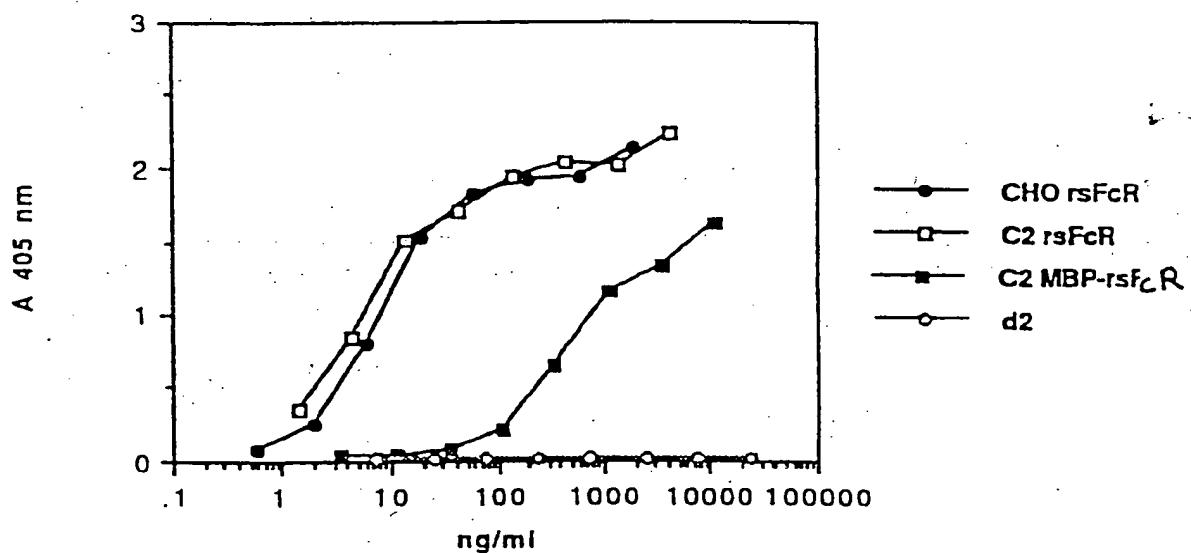


FIGURE 18

Human serum containing rheumatoid factors, but not normal human sera, inhibits the binding of HRP conjugated to rsHSA-Fc $\gamma$ RII to hagg.

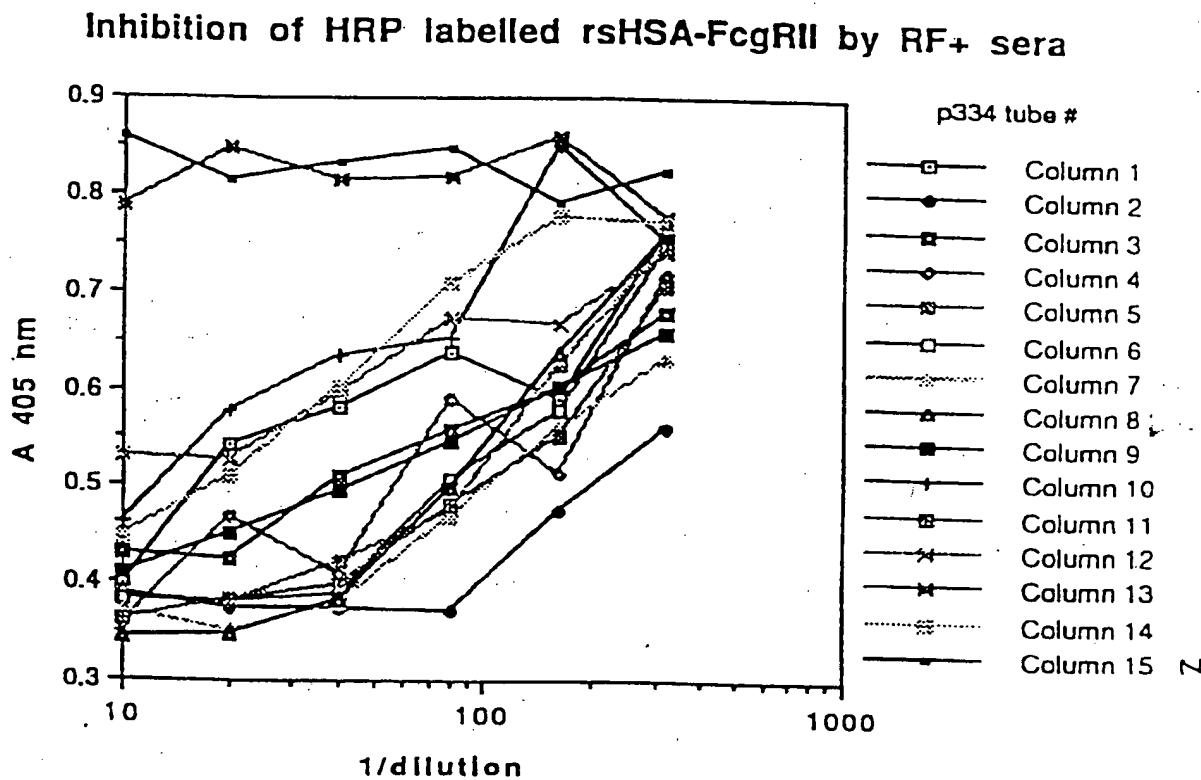


FIGURE 19

Peptoid name	A 405 nm (X 1000)	Peptoid name	A 405 nm (X 1000)
TC,1	308.5	NB,1	578.5
AD,1	317	BD,1	580
DC,1	319	OA,1	582.5
SC,1	319	DJ,1	586
AC,1	320	LG,1	586.5
RC,1	323.5	VF,1	586.5
NC,1	329.5	OG,1	587
UC,1	329.5	DS,1	587
LC,1	330.5	IF,1	588
FC,1	332.5	RA,1	588
JC,1	335	DL,1	589.5
HC,1	343	QB,1	591
QC,1	345.5	QF,1	592
GC,1	346.5	EU,1	592
CU,1	356	JE,1	592
MC,1	357	DQ,1	592.5
EC,1	358	AF,1	594
DG,1	359.5	SB,1	594
IC,1	363	HA,1	594.5
CF,1	363	IG,1	596
CG,1	364	HB,1	596.5
CV,1	364	DO,1	596.5
VC,1	364	RB,1	597
		Background	304
		Maximum	619